

#2

OIPE

RAW SEQUENCE LISTING

DATE: 12/12/2001

PATENT APPLICATION: US/10/005,907

TIME: 14:16:02

Input Set : A:\ES.txt

Output Set: N:\CRF3\12112001\I005907.raw

ENTERED

3 <110> APPLICANT: Union Chimique Belge, S.A.
 4 Nocka, Karl
 5 Pirozzi, Gregory
 6 Einstein, Richard
 8 <120> TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND
 MAST CELL
 9 ACTIVATION
 11 <130> FILE REFERENCE: 053529-5005
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/005,907
 C--> 13 <141> CURRENT FILING DATE: 2001-12-07
 13 <160> NUMBER OF SEQ ID NOS: 13
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 3762
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (25)..(432)
 25 <223> OTHER INFORMATION:
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 33 agt tgc ctg gga gag aat caa aag aag ccc aag aaa gga aac cca gat 99
 34 Ser Cys Leu Gly Glu Asn Gln Lys Lys Pro Lys Lys Gly Asn Pro Asp
 35 10 15 20 25
 37 gag gaa aga aaa cgg cag gaa atg act aca ttt gaa aga aaa ctt caa 147
 38 Glu Glu Arg Lys Arg Gln Glu Met Thr Thr Phe Glu Arg Lys Leu Gln
 39 30 35 40
 41 gat caa gat aag aaa agc caa gaa gtt tca tcc act tct aat cag gaa 195
 42 Asp Gln Asp Lys Lys Ser Gln Glu Val Ser Ser Thr Ser Asn Gln Glu
 43 45 50 55
 45 aac gag aat ggc agt ggt tct gaa gaa gtg tgc tac act gtc att aat 243
 46 Asn Glu Asn Gly Ser Gly Ser Glu Glu Val Cys Tyr Thr Val Ile Asn
 47 60 65 70
 49 cac atc ccc cat cag aga tcc tcc ctg agc tcc aat gat gat ggc tat 291
 50 His Ile Pro His Gln Arg Ser Ser Leu Ser Ser Asn Asp Asp Gly Tyr
 51 75 80 85
 53 gag aac att gac tcc ctc aca agg aaa gtg aga cag ttt aga gaa agg 339
 54 Glu Asn Ile Asp Ser Leu Thr Arg Lys Val Arg Gln Phe Arg Glu Arg
 55 90 95 100 105
 57 tca gag aca gaa tat gcc ctt ctt agg act tct gtt agt agg cct tgt 387
 58 Ser Glu Thr Glu Tyr Ala Leu Leu Arg Thr Ser Val Ser Arg Pro Cys
 59 110 115 120
 61 tcc tgc acc cat gag cat gat tat gaa gtt gtg ttt cca cac taa 432
 62 Ser Cys Thr His Glu His Asp Tyr Glu Val Val Phe Pro His
 63 125 130 135

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71	aatcatagaa	attgacacaa	tgacctaaaa	tattctatgt	gtttttgctt	gtaaagtttg	672
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75	tctaataccc	ctgactaaact	gaatggaccc	tcttctaggg	caaagagacc	tcagatgaac	792
77	ctgaaagact	gaattctggc	catgatagga	agggaggtga	gacacacctt	gttatacccc	852
79	ttcccttttg	gagtttatgc	acaagtgacc	aggatgagtc	ataagactga	tgaaatagac	912
81	tgattgtggc	aataagagtc	ccaattccaa	cctgactctg	gtgtagatca	cacactgtct	972
83	gagggattcc	atctatgaga	ctttgtctac	ataacagaga	ccttggtttc	cacaaccctt	1032
85	ttatttttagc	taaagcattc	ttttctactg	acttcttaag	tctttagaca	aagcttaact	1092
87	ctttcaacca	attggcaatc	agacaaactt	tgaactctac	tatgacctgt	aagctctctc	1152
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91	tgtctttgct	tgtaactcct	gtctccctaa	aatgtataaa	agtaaacggt	gacctgacca	1272
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113	aattcaagca	aactggaaaa	taatccatct	aattatgctt	tctttcccaa	gaagtttttt	1932
115	aatgatatgc	cagcttccct	atttggagac	aaaagcctta	attgacaatg	cattcattat	1992
117	atattttttt	gtatagttac	agtatacag	ttgagtatcc	cttagatgag	atgcttgagg	2052
119	ccagaagtgt	tttggatttc	agattttatt	ttggattttg	gaatatttcc	atacatataa	2112
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125	aacagagttt	gcgcacattg	gaccatcaga	aagcagaagt	gtcactattt	caagtcagtg	2292
127	ctcaaaaagt	ttcagatggt	aagctggtga	tgcagttcat	gccagtgatc	cgagtacttt	2352
129	gggaagccaa	gacaggtgga	tctcttgagc	ccaggagttt	gaggccagac	tgacacaac	2412
131	agtgagacct	cgtttctaca	aataattaaa	aaattagcca	ggtgtggtgg	tgacacacct	2472
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137	tcaaaaaaaa	aaaaaagttt	cagatttttg	agcatttccg	atcttcagat	tagggatttt	2652
139	caacctgtac	tgacctttta	gtcattgaca	agcattaatc	aataggtgga	ctccagataa	2712
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151	gtattgattg	gtagaaggaa	cgttgaaatc	caagagcatc	aatgtcttct	ggtggttcac	3072
153	cataagccac	agcagatgtc	ttaatctttc	cgagatctag	tttttcagca	aagcaggatt	3132
155	taagaaatgt	aactatctta	tgtggttatg	aagaacaata	gaatcattgc	tgtataagtg	3192
157	ctttttaact	tgtaaatttt	gtgaagctta	tcttttatgc	atataaatat	ttgaacattt	3252
159	tacattggtt	atatttttaa	tcagttttac	tcaagtgtga	ttatatacaa	gaaaatgtaa	3312
161	ccactgtaag	ggtagagtta	taagaatttt	gtcaaatgta	ttcacccatg	tagtcacctc	3372

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165 gagtttcacc agtcctggca accaatgata tgcttcgtat aattataact gttctagata 3492
167 tttgtagcaa tgtacccttt ccatatttat tttgtgtgtg taaggcttct tttagtcatt 3552
169 ataatatatt tgagattcat ctatgtttta tggtctatca gtagttgtac atcttacttg 3612
171 tctcagcata tcacatata gatatactat aatttggtta tctaactact gatggatatg 3672
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181 <213> ORGANISM: Homo sapiens
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193 Met Thr Thr Phe Glu Arg Lys Leu Gln Asp Gln Asp Lys Lys Ser Gln
194 35 40 45
197 Glu Val Ser Ser Thr Ser Asn Gln Glu Asn Glu Asn Gly Ser Gly Ser
198 50 55 60
201 Glu Glu Val Cys Tyr Thr Val Ile Asn His Ile Pro His Gln Arg Ser
202 65 70 75 80
205 Ser Leu Ser Ser Asn Asp Asp Gly Tyr Glu Asn Ile Asp Ser Leu Thr
206 85 90 95
209 Arg Lys Val Arg Gln Phe Arg Glu Arg Ser Glu Thr Glu Tyr Ala Leu
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213 Leu Arg Thr Ser Val Ser Arg Pro Cys Ser Cys Thr His Glu His Asp
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217 Tyr Glu Val Val Phe Pro His
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229 <223> OTHER INFORMATION: First ORF
232 <220> FEATURE:
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234 <222> LOCATION: (1238)..(2218)
235 <223> OTHER INFORMATION: Second ORF
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241 caggatctga gtgatgagac gtgtccccac tgaggtgccc cacagcagca ggtgttgagc 120
243 atgggctgag aagctggacc ggcaccaaag ggctggcaga aatgggcgcc tggtgattc 180
245 ctaggcagtt ggcggcagca aggaggagag gccgcagctt ctggagcaga gccgagacga 240
247 agcagttctg gagtgcctga acggccccct gagccctacc cgcttgccc act atg 296
248 Met

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249                                     1
251 gtc cag agg ctg tgg gtg agc cgc ctg ctg cgg cac cgg aaa gcc cag      344
252 Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln
253          5          10          15
255 ctc ttg ctg gtc aac ctg cta acc ttt ggc ctg gag gtg tgt ttg gcc      392
256 Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala
257          20          25          30
259 gca ggc atc acc tat gtg ccg cct ctg ctg ctg gaa gtg ggg gta gag      440
260 Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu
261          35          40          45
263 gag aag ttc atg acc atg gtg ctg ggt gag tca cta cat cct cct tcc      488
264 Glu Lys Phe Met Thr Met Val Leu Gly Glu Ser Leu His Pro Pro Ser
265 50          55          60          65
267 ttc ctg ttc cag ata cat gcc acc tgg cat gtg gga cag gag tac ctc      536
268 Phe Leu Phe Gln Ile His Ala Thr Trp His Val Gly Gln Glu Tyr Leu
269          70          75          80
271 tgc cct ggg agc tgc ttg gag gga gag gtg gtc tgc tgg gaa ggc att      584
272 Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly Ile
273          85          90          95
275 gct ggg cag gag ggt gac cct ggg ctg agg ggg cac acc aag aga aag      632
276 Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg Lys
277          100          105          110
279 aag aga ata cca agg aca tac ccc agt cac ctc tgg atc cct ggt cct      680
280 Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly Pro
281          115          120          125
283 gca cag agc ctg gct cat agg aga cac tgg aga aat gct cct aac ctt      728
284 Ala Gln Ser Leu Ala His Arg Arg His Trp Arg Asn Ala Pro Asn Leu
285 130          135          140          145
287 tgg cta gcc ctt tta taa tttatagcga ttatctcatt taatgcttac      776
288 Trp Leu Ala Leu Leu
289          150
291 aaccaccatt tgaggatc cattttacag agaaggaagc agaggctttt aagaggttag      836
293 gtaagtctta gccaaagcca aatagcagct gaacagtaga gctgggactc catcaaggctc      896
295 tcccagccgg agcttgetcc taccctagg acaaggggtg gactcctgac tctgcagata      956
297 aattctacaa aagccacaga aggcaagtag taaccattgt gtgacaaccc ctcaccccca      1016
299 ggaagagggg cccctgtgag gattgcaggc tctggagtca cactgcttgt tgaaacgctg      1076
301 cctcttacct tccctaggct tgcgcctttg aataagtatc acttcttagt tgctccatgc      1136
303 ctcatgttgt ccatctgaaa atgggggcat ctgtaatgcc tgtgttatga ggagtaaatt      1196
305 acagcatccc tgtgaagacg tagcacagtg tcgagtacgg a atg tta ttt cca tcc      1252
306                                     Met Leu Phe Pro Ser
307                                     155
309 ttc tca cgg agc ttg gtt ccc ctt ccc ctt gcc ctt tac ttg tcc cag      1300
310 Phe Ser Arg Ser Leu Val Pro Leu Pro Leu Ala Leu Tyr Leu Ser Gln
311          160          165          170
313 cca ttg act cat act act tcc ctt ctt gca ggc att ggt cca gtg ctg      1348
314 Pro Leu Thr His Thr Thr Ser Leu Leu Ala Gly Ile Gly Pro Val Leu
315          175          180          185
317 ggc ctg gtc tgt gtc ccg ctc cta ggc tca gcc agt gac cac tgg cgt      1396
318 Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg

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322	Gly Arg Tyr	Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly		
323	205	210	215	
325	atc ctg ctg agc ctc ttt ctc atc cca agg gcc ggc tgg cta gca ggg	1492		
326	Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly			
327	220	225	230	235
329	ctg ctg tgc ccg gat ccc agg ccc ctg gag ctg gca ctg ctc atc ctg	1540		
330	Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu			
331	240	245	250	
333	ggc gtg ggg ctg ctg gac ttc tgt ggc cag gtg tgc ttc act cca ctg	1588		
334	Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu			
335	255	260	265	
337	gag gcc ctg ctc tct gac ctc ttc cgg gac ccg gac cac tgt cgc cag	1636		
338	Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln			
339	270	275	280	
341	gcc tac tct gtc tat gcc ttc atg atc agt ctt ggg ggc tgc ctg ggc	1684		
342	Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly			
343	285	290	295	
345	tac ctc ctg cct gcc att gac tgg gac acc agt gcc ctg gcc ccc tac	1732		
346	Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr			
347	300	305	310	315
349	ctg ggc acc cag gag gag tgc ctc ttt ggc ctg ctc acc ctc atc ttc	1780		
350	Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe			
351	320	325	330	
353	ctc acc tgc gta gca gcc aca ctg ctg gtg gct gag gag gca gcg ctg	1828		
354	Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu			
355	335	340	345	
357	ggc ccc acc gag cca gca gaa ggg ctg tcg gcc ccc tcc ttg tcg ccc	1876		
358	Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro			
359	350	355	360	
361	cac tgc tgt cca tgc cag gcc cta agc ctg gag ctc cct tcc cta atg	1924		
362	His Cys Cys Pro Cys Gln Ala Leu Ser Leu Glu Leu Pro Ser Leu Met			
363	365	370	375	
365	gac acg tgg gtg ctg gag gca gtg gcc tgc tcc cac ctc cac ccg cgc	1972		
366	Asp Thr Trp Val Leu Glu Ala Val Ala Cys Ser His Leu His Pro Arg			
367	380	385	390	395
369	tct gcg ggg cct ctg cct gtg atg tct ccg tac gtg tgg tgg tgg gtg	2020		
370	Ser Ala Gly Pro Leu Pro Val Met Ser Pro Tyr Val Trp Trp Trp Val			
371	400	405	410	
373	agc cca ccg agg cca ggg tgg ttc cgg gcc ggg gca tct gcc tgg acc	2068		
374	Ser Pro Pro Arg Pro Gly Trp Phe Arg Ala Gly Ala Ser Ala Trp Thr			
375	415	420	425	
377	tcg cca tcc tgg ata gtg cct tcc tgc tgt ccc agg tgg ccc cat ccc	2116		
378	Ser Pro Ser Trp Ile Val Pro Ser Cys Cys Pro Arg Trp Pro His Pro			
379	430	435	440	
381	tgt tta tgg gct cca ttg tcc agc tca gcc agt ctg tca ctg cct ata	2164		
382	Cys Leu Trp Ala Pro Leu Ser Ser Ala Ser Leu Ser Leu Pro Ile			
383	445	450	455	

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date